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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/697,863A

DATE: 08/21/2002

TIME: 15:13:47

Input Set : A:\2676-4555 seq listing v2.ST25.txt

Output Set: N:\CRF4\08212002\I697863A.raw

3 <110> APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
 5 <120> TITLE OF INVENTION: CD-40 INTERACTING AND TRAF-INTERACTING PROTEINS
 7 <130> FILE REFERENCE: 2676-4555US
 9 <140> CURRENT APPLICATION NUMBER: US 09/697,863A
 10 <141> CURRENT FILING DATE: 2000-10-27
 12 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03025
 13 <151> PRIOR FILING DATE: 1999-04-28
 15 <150> PRIOR APPLICATION NUMBER: EPO 98201392.2
 16 <151> PRIOR FILING DATE: 1998-04-29
 18 <160> NUMBER OF SEQ ID NOS: 6
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1920
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: misc_feature
 29 <222> LOCATION: (1627)..(1627)
 30 <223> OTHER INFORMATION: N stands for any nucleotide.
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (20)..(1108)
 36 <223> OTHER INFORMATION:
 38 <220> FEATURE:
 39 <221> NAME/KEY: misc_feature
 40 <222> LOCATION: (1849)..(1849)
 41 <223> OTHER INFORMATION: N stands for any nucleotide.
 44 <400> SEQUENCE: 1
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 46 Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg
 47 1 5 10
 49 gag gcg gcg gag gaa gag ggc gag cct gag gtg aaa aag cgg cga ctt 100
 50 Glu Ala Ala Glu Glu Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu
 51 15 20 25
 53 ctg tgt gtg gag ttt gcc tcg gtc gca agc tgc gat gcc gca gtg gct 148
 54 Leu Cys Val Glu Phe Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala
 55 30 35 40
 57 cag tgc ttc ctg gcc gag aac gac tgg gag atg gaa agg gct ctg aac 196
 58 Gln Cys Phe Leu Ala Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn
 59 45 50 55
 61 tcc tac ttc gag cct ccg gtg gag gag agc gcc ttg gaa cgc cga cct 244
 62 Ser Tyr Phe Glu Pro Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro
 63 60 65 70 75

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65	gaa acc atc tct gag ccc aag acc tat gtt gac cta acc aat gaa gaa	292
66	Glu Thr Ile Ser Glu Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu	
67	80 85 90	
69	aca act gat tcc acc act tct aaa atc agc cca tct gaa gat act cag	340
70	Thr Thr Asp Ser Thr Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln	
71	95 100 105	
73	caa gaa aat ggc agc atg ttc tct ctc att acc tgg aat att gat gga	388
74	Gln Glu Asn Gly Ser Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly	
75	110 115 120	
77	tta gat cta aac aat ctg tca gag agg gct cga ggg gtg tgt tcc tac	436
78	Leu Asp Leu Asn Asn Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr	
79	125 130 135	
81	tta gct ttg tac agc cca gat gtg ata ttt cta cag gaa gtt att ccc	484
82	Leu Ala Leu Tyr Ser Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro	
83	140 145 150 155	
85	cca tat tat agc tac cta aag aag aga tca agt aat tat gag att att	532
86	Pro Tyr Tyr Ser Tyr Leu Lys Lys Arg Ser Ser Asn Tyr Glu Ile Ile	
87	160 165 170	
89	aca ggt cat gaa gaa gga tat ttc aca gct ata atg ttg aag aaa tca	580
90	Thr Gly His Glu Glu Gly Tyr Phe Thr Ala Ile Met Leu Lys Lys Ser	
91	175 180 185	
93	aga gtg aaa tta aaa agc caa gag att att cct ttt cca agt acc aaa	628
94	Arg Val Lys Leu Lys Ser Gln Glu Ile Ile Pro Phe Pro Ser Thr Lys	
95	190 195 200	
97	atg atg aga aac ctt tta tgt gtg cat gtg aat gtg tca gga aat gag	676
98	Met Met Arg Asn Leu Leu Cys Val His Val Asn Val Ser Gly Asn Glu	
99	205 210 215	
101	ctt tgc ctt atg aca tcc cat ttg gag agc acc aga ggg cat gct gcg	724
102	Leu Cys Leu Met Thr Ser His Leu Glu Ser Thr Arg Gly His Ala Ala	
103	220 225 230 235	
105	gaa cga atg aat cag tta aaa atg gtt tta aag aaa atg caa gag gct	772
106	Glu Arg Met Asn Gln Leu Lys Met Val Leu Lys Lys Met Gln Glu Ala	
107	240 245 250	
109	cca gag tca gct aca gtt ata ttt gca gga gat aca aat cta agg gat	820
110	Pro Glu Ser Ala Thr Val Ile Phe Ala Gly Asp Thr Asn Leu Arg Asp	
111	255 260 265	
113	cga gag gtt acc aga tgt ggt ggt tta ccc aac aac att gtg gat gtc	868
114	Arg Glu Val Thr Arg Cys Gly Gly Leu Pro Asn Asn Ile Val Asp Val	
115	270 275 280	
117	tgg gag ttt ttg ggc aaa cct aaa cat tgc cag tat aca tgg gat aca	916
118	Trp Glu Phe Leu Gly Lys Pro Lys His Cys Gln Tyr Thr Trp Asp Thr	
119	285 290 295	
121	caa atg aac tct aat ctt gga ata act gct gct tgt aaa ctt cgt ttt	964
122	Gln Met Asn Ser Asn Leu Gly Ile Thr Ala Ala Cys Lys Leu Arg Phe	
123	300 305 310 315	
125	gat cga ata ttt ttc aga gca gca gca gaa gag gga cac att att ccc	1012
126	Asp Arg Ile Phe Phe Arg Ala Ala Ala Glu Glu Gly His Ile Ile Pro	
127	320 325 330	
129	cga agt ttg gac ctt ctt gga tta gaa aaa ctg gac tgt ggt aga ttt	1060

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130 Arg Ser Leu Asp Leu Leu Gly Leu Glu Lys Leu Asp Cys Gly Arg Phe
131          335          340          345
133 cct agt gat cac tgg ggt ott ctg tgc aac tta gat ata ata ttg taa      1108
134 Pro Ser Asp His Trp Gly Leu Leu Cys Asn Leu Asp Ile Ile Leu
135          350          355          360
137 aatgcttttc aagtgtgggt tttgccctga ttgttgcaaa tacaatttcc accttctgga      1168
139 aaggtagggt tgctgtggag gaaataatgt actagatcat tgtcacagaa aaaccaacta      1228
141 tgatttatgg ttgtgttttc agaattcaac attaaagatt aatgtttatt taaacgaaca      1288
143 cattcctgca ttcaggatgt gaggccattt aataaaaagg gcacaaagcc tgtcagagtt      1348
145 ttcaacggtg cttacagctg ccagctggat tccaaacagg taccocattg tctctgagct      1408
147 aatgtttata tttttccatt caggcaccga aatagttaat atttaaaata agtcttcaaa      1468
149 agaaaacata agagattatt gagttcttgg gactggatcc tttatttcat aagttcagat      1528
151 catcttaaat gaaaatgcc aagattatctg cagttaagta gatgacagct attctacatc      1588
W--> 153 agacttgatt ttgtcagct aattacataa ttggtaagnt ataattgaaa ccttatggct      1648
155 taaaattcct taactccttt ttgattcatg ttgtagtca tgttgtcaac agaggcaaag      1708
157 ttaagcttga tgatggttaa aatcggtttg atagcaccat gggacatttt tttaacaaaa      1768
159 ataaatgcat gaagagacat agccttttag ttttgctaat tgtgaaatgg aaatgcttta      1828
W--> 161 caggaagtaa atgcaaatta nttttaagtg tgctttaaag aaaaatattt tccccacagg      1888
163 agaaatttaa ataaagaatt ttatttggt a a                                1920
166 <210> SEQ ID NO: 2
167 <211> LENGTH: 362
168 <212> TYPE: PRT
169 <213> ORGANISM: Homo sapiens
171 <400> SEQUENCE: 2
173 Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu
174 1          5          10          15
177 Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Val Glu Phe
178          20          25          30
181 Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala
182          35          40          45
185 Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro
186          50          55          60
189 Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Glu Thr Ile Ser Glu
190 65          70          75          80
193 Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu Thr Thr Asp Ser Thr
194          85          90          95
197 Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln Gln Glu Asn Gly Ser
198          100         105         110
201 Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly Leu Asp Leu Asn Asn
202          115         120         125
205 Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr Leu Ala Leu Tyr Ser
206          130         135         140
209 Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro Pro Tyr Tyr Ser Tyr
210 145         150         155         160
213 Leu Lys Lys Arg Ser Ser Asn Tyr Glu Ile Ile Thr Gly His Glu Glu
214          165         170         175
217 Gly Tyr Phe Thr Ala Ile Met Leu Lys Lys Ser Arg Val Lys Leu Lys
218          180         185         190
221 Ser Gln Glu Ile Ile Pro Phe Pro Ser Thr Lys Met Met Arg Asn Leu

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222          195          200          205
225 Leu Cys Val His Val Asn Val Ser Gly Asn Glu Leu Cys Leu Met Thr
226          210          215          220
229 Ser His Leu Glu Ser Thr Arg Gly His Ala Ala Glu Arg Met Asn Gln
230 225          230          235          240
233 Leu Lys Met Val Leu Lys Lys Met Gln Glu Ala Pro Glu Ser Ala Thr
234          245          250          255
237 Val Ile Phe Ala Gly Asp Thr Asn Leu Arg Asp Arg Glu Val Thr Arg
238          260          265          270
241 Cys Gly Gly Leu Pro Asn Asn Ile Val Asp Val Trp Glu Phe Leu Gly
242          275          280          285
245 Lys Pro Lys His Cys Gln Tyr Thr Trp Asp Thr Gln Met Asn Ser Asn
246          290          295          300
249 Leu Gly Ile Thr Ala Ala Cys Lys Leu Arg Phe Asp Arg Ile Phe Phe
250 305          310          315          320
253 Arg Ala Ala Ala Glu Glu Gly His Ile Ile Pro Arg Ser Leu Asp Leu
254          325          330          335
257 Leu Gly Leu Glu Lys Leu Asp Cys Gly Arg Phe Pro Ser Asp His Trp
258          340          345          350
261 Gly Leu Leu Cys Asn Leu Asp Ile Ile Leu
262          355          360
265 <210> SEQ ID NO: 3
266 <211> LENGTH: 1312
267 <212> TYPE: DNA
268 <213> ORGANISM: Mus musculus
270 <220> FEATURE:
271 <221> NAME/KEY: CDS
272 <222> LOCATION: (122)..(1234)
273 <223> OTHER INFORMATION:
275 <400> SEQUENCE: 3
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277 aattcggcac gagggcgga agcagcgtga agagcgggtg ttttgagggg accctgcggc      120
278 g atg gcg tct ggc agc agt tcc gat gcg gcg gag ccc gca ggg ccg gca      169
281 Met Ala Ser Gly Ser Ser Ser Asp Ala Ala Glu Pro Ala Gly Pro Ala
282 1 5 10 15
284 ggg cgg gcg gcg tgg gcg ccc gaa gca gca cag gcg gag gag gac cgg      217
285 Gly Arg Ala Ala Ser Ala Pro Glu Ala Ala Gln Ala Glu Glu Asp Arg
286 20 25 30
288 gtg aag agg cgg cgg ctt cag tgc ctg ggc ttt gcg ttg gtg ggg gga      265
289 Val Lys Arg Arg Arg Leu Gln Cys Leu Gly Phe Ala Leu Val Gly Gly
290 35 40 45
292 tgc gac ccc acg atg gtc ccc agc gtc ctg cgg gag aac gac tgg cag      313
293 Cys Asp Pro Thr Met Val Pro Ser Val Leu Arg Glu Asn Asp Trp Gln
294 50 55 60
296 acg cag aaa gcc ctg agc gcc tac ttc gag ctg cca gag aac gac caa      361
297 Thr Gln Lys Ala Leu Ser Ala Tyr Phe Glu Leu Pro Glu Asn Asp Gln
298 65 70 75 80
300 ggg tgg ccg cgc cag cct ccc acg tcc ttc aag tcc gag gcc tat gtt      409
301 Gly Trp Pro Arg Gln Pro Pro Thr Ser Phe Lys Ser Glu Ala Tyr Val

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302		85		90		95		
304	gat cta acc aac gag gat gca aat gat aca acc att tta gaa gcc agt							457
305	Asp Leu Thr Asn Glu Asp Ala Asn Asp Thr Thr Ile Leu Glu Ala Ser							
306		100		105		110		
308	cca tct gga act cct cta gaa gat agc agc act att tct ttc att acc							505
309	Pro Ser Gly Thr Pro Leu Glu Asp Ser Ser Thr Ile Ser Phe Ile Thr							
310		115		120		125		
312	tgg aat att gat gga tta gat gga tgc aat ctg ccc gag agg gct cga							553
313	Trp Asn Ile Asp Gly Leu Asp Gly Cys Asn Leu Pro Glu Arg Ala Arg							
314		130		135		140		
316	ggg gtg tgt tcc tgc cta gct ttg tat agt cca gat gtg gta ttt cta							601
317	Gly Val Cys Ser Cys Leu Ala Leu Tyr Ser Pro Asp Val Val Phe Leu							
318		145		150		155		160
320	cag gaa gtt atc ccc cca tac tgt gcc tac cta aag aag aga gca gcc							649
321	Gln Glu Val Ile Pro Pro Tyr Cys Ala Tyr Leu Lys Lys Arg Ala Ala							
322		165		170		175		
324	agt tac aca att att aca ggt aat gaa gaa gga tat ttc aca gct ata							697
325	Ser Tyr Thr Ile Ile Thr Gly Asn Glu Glu Gly Tyr Phe Thr Ala Ile							
326		180		185		190		
328	cta ttg aag aaa gga aga gtg aaa ttt aaa agt cag gag att att cct							745
329	Leu Leu Lys Lys Gly Arg Val Lys Phe Lys Ser Gln Glu Ile Ile Pro							
330		195		200		205		
332	ttt cca aat acc aaa atg atg aga aac ctg cta tgc gta aat gtg agt							793
333	Phe Pro Asn Thr Lys Met Met Arg Asn Leu Leu Cys Val Asn Val Ser							
334		210		215		220		
336	ttg ggt gga aat gaa ttt tgc ctt atg aca tcc cat ttg gag agc acc							841
337	Leu Gly Gly Asn Glu Phe Cys Leu Met Thr Ser His Leu Glu Ser Thr							
338		225		230		235		240
340	aga gaa cat tct gcg gaa cga ata aga caa tta aaa act gtt ctt gga							889
341	Arg Glu His Ser Ala Glu Arg Ile Arg Gln Leu Lys Thr Val Leu Gly							
342		245		250		255		
344	aaa atg caa gag gct cca gat tca acc acg gtt ata ttt gca gga gat							937
345	Lys Met Gln Glu Ala Pro Asp Ser Thr Thr Val Ile Phe Ala Gly Asp							
346		260		265		270		
348	aca aat tta aga gat caa gaa gtt atc aaa tgt ggt ggt tta cct gac							985
349	Thr Asn Leu Arg Asp Gln Glu Val Ile Lys Cys Gly Gly Leu Pro Asp							
350		275		280		285		
352	aac gtt ttt gat gcc tgg gaa ttt tta ggc aaa cct aaa cat tgc cag							1033
353	Asn Val Phe Asp Ala Trp Glu Phe Leu Gly Lys Pro Lys His Cys Gln							
354		290		295		300		
356	tat aca tgg gat acg aaa gca aat aac aac ctc agg atc cct gct gct							1081
357	Tyr Thr Trp Asp Thr Lys Ala Asn Asn Asn Leu Arg Ile Pro Ala Ala							
358		305		310		315		320
360	tat aag cat cgt ttt gat cga ata ttt ttc aga gca gaa gag ggg cac							1129
361	Tyr Lys His Arg Phe Asp Arg Ile Phe Phe Arg Ala Glu Glu Gly His							
362		325		330		335		
364	ctt att cct caa agt tta gac ctt gtt ggg ttg gaa aaa ctg gac tgt							1177
365	Leu Ile Pro Gln Ser Leu Asp Leu Val Gly Leu Glu Lys Leu Asp Cys							
366		340		345		350		

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/21/2002
PATENT APPLICATION: US/09/697,863A TIME: 15:13:48

Input Set : A:\2676-4555 seq listing v2.ST25.txt
Output Set: N:\CRF4\08212002\I697863A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1627,1849
Seq#:5; N Pos. 1392,1530,1531
Seq#:5; Xaa Pos. 395,441
Seq#:6; Xaa Pos. 395,441

VERIFICATION SUMMARY

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Output Set: N:\CRF4\08212002\I697863A.raw

L:153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1588
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1828
L:611 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1384
L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1432
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1528
L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1536
L:742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:384
L:754 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:432